



# UNITED STATES PATENT AND TRADEMARK OFFICE

UNITED STATES DEPARTMENT OF COMMERCE  
United States Patent and Trademark Office  
Address: COMMISSIONER FOR PATENTS  
P.O. Box 1450  
Alexandria, Virginia 22313-1450  
www.uspto.gov

APPLICATION NO.	FILING DATE	FIRST NAMED INVENTOR	ATTORNEY DOCKET NO.	CONFIRMATION NO.
-----------------	-------------	----------------------	---------------------	------------------

10/523,143

08/16/2005

Eric E Schadt

9301-211-999

6414

20583

7590

11/02/2009

JONES DAY  
222 EAST 41ST ST  
NEW YORK, NY 10017

EXAMINER

BRUSCA, JOHN S

ART UNIT

PAPER NUMBER

1631

MAIL DATE

DELIVERY MODE

11/02/2009

PAPER

**Please find below and/or attached an Office communication concerning this application or proceeding.**

The time period for reply, if any, is set in the attached communication.

<b>Office Action Summary</b>	<b>Application No.</b> 10/523,143	<b>Applicant(s)</b> SCHADT ET AL.	
	<b>Examiner</b> John S. Brusca	<b>Art Unit</b> 1631	

-- The MAILING DATE of this communication appears on the cover sheet with the correspondence address --

### Period for Reply

A SHORTENED STATUTORY PERIOD FOR REPLY IS SET TO EXPIRE 3 MONTH(S) OR THIRTY (30) DAYS, WHICHEVER IS LONGER, FROM THE MAILING DATE OF THIS COMMUNICATION.

- Extensions of time may be available under the provisions of 37 CFR 1.136(a). In no event, however, may a reply be timely filed after SIX (6) MONTHS from the mailing date of this communication.
- If NO period for reply is specified above, the maximum statutory period will apply and will expire SIX (6) MONTHS from the mailing date of this communication.
- Failure to reply within the set or extended period for reply will, by statute, cause the application to become ABANDONED (35 U.S.C. § 133). Any reply received by the Office later than three months after the mailing date of this communication, even if timely filed, may reduce any earned patent term adjustment. See 37 CFR 1.704(b).

### Status

- 1) ☒ Responsive to communication(s) filed on 06 August 2009.
- 2a) ☒ This action is **FINAL**. 2b) ☐ This action is non-final.
- 3) ☐ Since this application is in condition for allowance except for formal matters, prosecution as to the merits is closed in accordance with the practice under *Ex parte Quayle*, 1935 C.D. 11, 453 O.G. 213.

### Disposition of Claims

- 4) ☒ Claim(s) 1-21, 23-25, 28-30, 33, 35-37, 40-50, 52-54, 107, 252, 253 and 258-262 is/are pending in the application.
- 4a) Of the above claim(s) \_\_\_\_\_ is/are withdrawn from consideration.
- 5) ☐ Claim(s) \_\_\_\_\_ is/are allowed.
- 6) ☒ Claim(s) 1-21, 23-25, 28-30, 33, 35-37, 40-50, 52-54, 107, 252, 253, and 258-262 is/are rejected.
- 7) ☐ Claim(s) \_\_\_\_\_ is/are objected to.
- 8) ☐ Claim(s) \_\_\_\_\_ are subject to restriction and/or election requirement.

### Application Papers

- 9) ☐ The specification is objected to by the Examiner.
- 10) ☐ The drawing(s) filed on \_\_\_\_\_ is/are: a) ☐ accepted or b) ☐ objected to by the Examiner.  
Applicant may not request that any objection to the drawing(s) be held in abeyance. See 37 CFR 1.85(a).  
Replacement drawing sheet(s) including the correction is required if the drawing(s) is objected to. See 37 CFR 1.121(d).
- 11) ☐ The oath or declaration is objected to by the Examiner. Note the attached Office Action or form PTO-152.

### Priority under 35 U.S.C. § 119

- 12) ☐ Acknowledgment is made of a claim for foreign priority under 35 U.S.C. § 119(a)-(d) or (f).
- a) ☐ All b) ☐ Some \* c) ☐ None of:
- ☐ Certified copies of the priority documents have been received.
  - ☐ Certified copies of the priority documents have been received in Application No. \_\_\_\_\_.
  - ☐ Copies of the certified copies of the priority documents have been received in this National Stage application from the International Bureau (PCT Rule 17.2(a)).

\* See the attached detailed Office action for a list of the certified copies not received.

### Attachment(s)

- |  |   |
|--|---|
| 1) <input type="checkbox"/> Notice of References Cited (PTO-892)                     | 4) <input type="checkbox"/> Interview Summary (PTO-413)           |
| 2) <input type="checkbox"/> Notice of Draftsperson's Patent Drawing Review (PTO-948) | Paper No(s)/Mail Date. _____                                      |
| 3) <input type="checkbox"/> Information Disclosure Statement(s) (PTO/SB/08)          | 5) <input type="checkbox"/> Notice of Informal Patent Application |
| Paper No(s)/Mail Date _____  | 6) <input type="checkbox"/> Other: _____                          |

## **DETAILED ACTION**

### ***Status of the Claims***

1. Claims 1-21, 23-25, 28-30, 33, 35-37, 40-50, 52-54, 107, 252, 253, and 258-262 are pending.
2. Claims 1-21, 23-25, 28-30, 33, 35-37, 40-50, 52-54, 107, 252, 253, and 258-262 are rejected.

### ***Specification***

3. The objection to the specification in the Office action mailed 12 February 2009 is withdrawn in view of the amendment to the specification filed 06 August 2009.

### ***Claim Rejections - 35 USC § 101***

4. The rejection of claims 1-25, 28-30, 33-37, 40-50, 52-53, 252, 253, and 258-262 under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter due to claimed subject matter that is a process not limited to using a machine or producing a transformation is withdrawn in view of the amendment to the claims and arguments filed 06 August 2009 that independent claims 1, 54, and 107 are either processes that use a machine or are limited to machines.
5. The rejection of claims 1-25, 28-30, 33-37, 40-50, 52-54, 107, 252, 253, and 258-262 under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter due to lack of a practical application of an abstract idea is withdrawn in view of the arguments presented in the response filed 06 August 2009.

Art Unit: 1631

6. The rejection of claim 54 under 35 U.S.C. 101 because the claimed invention is directed to non-statutory subject matter due to embodiments that are not a machine is withdrawn in view of the arguments filed 06 August 2009.

***Claim Rejections - 35 USC § 112***

7. The following is a quotation of the second paragraph of 35 U.S.C. 112:

The specification shall conclude with one or more claims particularly pointing out and distinctly claiming the subject matter which the applicant regards as his invention.

8. Claims 259-261 are rejected under 35 U.S.C. 112, second paragraph, as being indefinite for failing to particularly point out and distinctly claim the subject matter which applicant regards as the invention.

Claims 259-261 are indefinite because all variables in the claims are not defined, nor is there a limiting definition for such variables in the specification. This indefiniteness precludes rejection under 35 102 or 103 until the meaning of all variables are made clear.

9. Applicant's arguments filed 06 August 2009 have been fully considered but they are not persuasive. The applicants have not amended the claims to define each variable in the equations recited in the claims (for example,  $y_1$  and  $y_2$ ), and therefore the claims remain indefinite.

***Claim Rejections - 35 USC § 102***

10. The following is a quotation of the appropriate paragraphs of 35 U.S.C. 102 that form the basis for the rejections under this section made in this Office action:

A person shall be entitled to a patent unless –

Art Unit: 1631

(b) the invention was patented or described in a printed publication in this or a foreign country or in public use or on sale in this country, more than one year prior to the date of application for patent in the United States.

11. Claims 1, 2, 5-11, 42-44, 49, 50, 52, 53, 252, and 258 are rejected under 35 U.S.C. 102(b) as being anticipated by Aitman et al. (cited as reference C01 in the Information Disclosure Statement filed 06 March 2006, Nature Genetics Vol. 21, pages 76-83 (1999)).

The claims are drawn to a method of measuring an expression quantitative trait locus (eQTL), a clinical quantitative trait locus (cQTL), and determining whether the gene assayed in the determination of the eQTL and the clinical trait are associated by determining if the eQTL and cQTL map to the same locus. In some embodiments the gene assayed in the determination of the eQTL maps to the locus of the cQTL, the eQTL and cQTL are the same pleiotropic QTL, the analysis uses genetic maps reflecting the genotype of an individual, the analysis uses restriction fragment length polymorphisms, the analysis uses pedigree data and F2 populations, the trait is a complex trait with incomplete penetrance, some individuals do not have an allele that predisposes to a disease trait, the complex trait is diabetes, the eQTL and cQTL are colocalized within 6 centimorgans (cM), genetic linkage is observed between the eQTL and the cQTL, and the eQTL and the cQTL are shown to be a common QTL and are not merely in linkage disequilibrium (i.e., closely linked).

Aitman et al. shows in the abstract a method of genetically analyzing complex disorders such as diabetes by correlating a QTL for different traits of diabetes (insulin-mediated glucose uptake and catecholamine-mediated lipolysis) with mapping of the expression trait for the gene

Art Unit: 1631

Cd36. Aitman et al. used spontaneously hypertensive rat (SHR) animals as the phenotype that was mapped by both eQTL and cQTL. Aitman et al. maps insulin-mediated glucose uptake and catecholamine-mediated lipolysis to a region near the microsatellite marker D4Bro1 on pages 76-77, which is a determination of a cQTL. Figure 2 and the discussion on pages 77-78 show the analysis of cDNA by expression level microarrays that determines an eQTL that correlates with SHR individuals. The identified eQTL is from the Cd36 gene. Cd36 is mapped to a region near the D4Bro1 site in figures 3 and pages 78-79 (using radiation hybrids to a precision of about 1cM with a Lod of 5.1 to 9.6 for the intervals measured). Aitman et al. employs F2 crossed rats to map insulin-mediated glucose uptake and catecholamine-mediated lipolysis on page 79 to Cd36, which is a determination of a cQTL that colocalizes with the eQTL determined on page 78. Page 79 and figure 7 show that Cd36 mutations correlate with the trait and that a normal and an affected strain differ by a duplication or deletion of the Cd36 gene. Figure 1 and column 1 on page 77 show that the phenotype in affected individuals has partial penetrance in affecting glucose uptake.

***Claim Rejections - 35 USC § 103***

12. The following is a quotation of 35 U.S.C. 103(a) which forms the basis for all obviousness rejections set forth in this Office action:

(a) A patent may not be obtained though the invention is not identically disclosed or described as set forth in section 102 of this title, if the differences between the subject matter sought to be patented and the prior art are such that the subject matter as a whole would have been obvious at the time the invention was made to a person having ordinary skill in the art to which said subject matter pertains. Patentability shall not be negated by the manner in which the invention was made.

Art Unit: 1631

This application currently names joint inventors. In considering patentability of the claims under 35 U.S.C. 103(a), the examiner presumes that the subject matter of the various claims was commonly owned at the time any inventions covered therein were made absent any evidence to the contrary. Applicant is advised of the obligation under 37 CFR 1.56 to point out the inventor and invention dates of each claim that was not commonly owned at the time a later invention was made in order for the examiner to consider the applicability of 35 U.S.C. 103(c) and potential 35 U.S.C. 102(e), (f) or (g) prior art under 35 U.S.C. 103(a).

13. Claims 1 and 12-16 are rejected under 35 U.S.C. 103(a) as being unpatentable over Aitman et al.

The claims are drawn to a method of measuring an expression quantitative trait locus (eQTL), a clinical quantitative trait locus (cQTL), and determining whether the gene assayed in the determination of the eQTL and the clinical trait are associated by determining if the eQTL and cQTL map to the same locus. In some embodiments the eQTL is determined from a normalized expression value, the expression level is determined by measurement of an mRNA by use of a microarray, and the normalization is done by either a normalization gene set, a ratio median correction, or a background correction.

Aitman et al. shows in the abstract a method of genetically analyzing complex disorders such as diabetes by correlating a QTL for different traits of diabetes (insulin-mediated glucose uptake and catecholamine-mediated lipolysis) with mapping of the expression trait for the gene Cd36. Aitman et al. used spontaneously hypertensive rat (SHR) animals as the phenotype that was mapped by both eQTL and cQTL. Aitman et al. maps insulin-mediated glucose uptake and catecholamine-mediated lipolysis to a region near the microsatellite marker D4Bro1 on pages 76-

Art Unit: 1631

77, which is a determination of a cQTL. Figure 2 and the discussion on pages 77-78 show the analysis of cDNA by expression level microarrays that determines an eQTL that correlates with SHR individuals. The identified eQTL is from the Cd36 gene. Cd36 is mapped to a region near the D4Bro1 site in figures 3 and pages 78-79 (using radiation hybrids to a precision of about 1cM with a Lod of 5.1 to 9.6 for the intervals measured). Aitman et al. employs F2 crossed rats to map insulin-mediated glucose uptake and catecholamine-mediated lipolysis on page 79 to Cd36, which is a determination of a cQTL that colocalizes with the eQTL determined on page 78. Page 79 and figure 7 show that Cd36 mutations correlate with the trait and that a normal and an affected strain differ by a duplication or deletion of the Cd36 gene. Figure 1 and column 1 on page 77 show that the phenotype in affected individuals has partial penetrance in affecting glucose uptake. Aitman et al. shows on page 82 that the microarray comprises control probes for housekeeping genes, and synthetic, yeast, and human probes that would not be expected to hybridize the rat cDNA samples. Two differently fluorophore labeled samples from different rat strains were simultaneously applied to the microarray, and the ratios of hybridization were determined for each probe on the microarray.

Aitman et al. does not discuss how the raw data of the microarray was processed to give the final expression ratios reported on page 77.

It would have been obvious to a person of ordinary skill in the art at the time the invention was made to process the raw data of the microarray of Aitman et al. by subtracting background hybridization levels by use of the non-homologous probe signal levels included in the microarray as controls, and it would be further obvious to convert the levels of each measured fluorophore for each probe as a ratio of signals rather than two raw signals because



Art Unit: 1631

Aitman et al. is interested in determining the relative levels of expression of every measured gene in the two compared strains, as reported on page 77 of Aitman et al.

14. Claims 1, 3, 4, 17-21, 23-25, 28-30, 33, 35-37, 40, 41, and 45-49 are rejected under 35 U.S.C. 103(a) as being unpatentable over Aitman et al. in view of Dominiczak et al. (Hypertension Vol. 35 (part 2), pages 164-172 (2000))

The claims are drawn to a method of measuring an expression quantitative trait locus (eQTL), a clinical quantitative trait locus (cQTL), and determining whether the gene assayed in the determination of the eQTL and the clinical trait are associated by determining if the eQTL and cQTL map to the same locus. In some embodiments the eQTL and cQTL are colocalized within 1 centimorgan (cM). In some embodiments either the eQTL linkage or the cQTL linkage is tested at a plurality of positions in the genome with a precision of at least 2.5 cM, and a statistical score for the linkage is determined that is a Lod score of greater than 5.0. In some embodiments the individual is a human. In some embodiments the complex trait is the effect of a mutation in a plurality of genes, the complex has a high frequency of disease causing alleles, the trait does not exhibit Mendelian inheritance, or the trait is hypertension.

Aitman et al. shows in the abstract a method of genetically analyzing complex disorders such as diabetes by correlating a QTL for different traits of diabetes (insulin-mediated glucose uptake and catecholamine-mediated lipolysis) with mapping of the expression trait for the gene Cd36. Aitman et al. used spontaneously hypertensive rat (SHR) animals as the phenotype that was mapped by both eQTL and cQTL. Aitman et al. maps insulin-mediated glucose uptake and catecholamine-mediated lipolysis to a region near the microsatellite marker D4Bro1 on pages 76-77, which is a determination of a cQTL. Figure 2 and the discussion on pages 77-78 show the

Art Unit: 1631

analysis of cDNA by expression level microarrays that determines an eQTL that correlates with SHR individuals. The identified eQTL is from the Cd36 gene. Cd36 is mapped to a region near the D4Bro1 site in figures 3 and pages 78-79 (using radiation hybrids to a precision of about 1cM with a Lod of 5.1 to 9.6 for the intervals measured). Aitman et al. employs F2 crossed rats to map insulin-mediated glucose uptake and catecholamine-mediated lipolysis on page 79 to Cd36, which is a determination of a cQTL that colocalizes with the eQTL determined on page 78. Page 79 and figure 7 show that Cd36 mutations correlate with the trait and that a normal and an affected strain differ by a duplication or deletion of the Cd36 gene. Figure 1 and column 1 on page 77 show that the phenotype in affected individuals has partial penetrance in affecting glucose uptake. Aitman et al. shows use of congenic rats to map QTL with higher precision than that achieved by F2 analysis.

Aitman et al. does not show mapping of a QTL with a precision of 1 cM, or determining whether a QTL maps to a plurality of positions in a genome. Aitman et al. does not show analysis of a human QTL. Aitman et al. does not show analysis of a trait affected by a plurality of mutations in different genes, or a high frequency of disease causing alleles, or non-Mendelian inheritance (limited penetrance) of a trait, or a trait that is hypertension.

Dominiczak et al. reviews the genetics of hypertension. Dominiczak et al. shows on the first column of page 165 that human genes have been identified that contribute to hypertension (a quantitative trait) with a Lod score of greater than 2. Table 1 shows rat loci and alleles that confer hypertension in strains that contain the allele. The alleles are on different chromosomes, and contribute to hypertension with Lod scores ranging from 3.0 to 16.6. Dominiczak et al. notes the work of Aitman et al. on page 167 as being an important advance in genetic analysis of

Art Unit: 1631

disease traits. Dominiczak et al. shows on pages 167 through 169 the use of congenic strains to map a QTL. Dominiczak et al. shows on page 169 that more refined mapping to a precision of 1 cM is desirable for positional cloning of desired loci, which requires substitution mapping and knowledge of high density polymorphic markers.

It would have been obvious to a person of ordinary skill in the art at the time the invention was made to modify the analysis of Aitman et al. by analyzing human QTL markers, and to more precisely map the analyzed QTL markers, and to extend the analysis to a plurality of QTL markers with limited penetrance because Dominiczak et al. shows that hypertension is caused by a plurality of limited penetrance alleles at different loci. It would have been further obvious to map the QTL markers with higher precision because Dominiczak et al. state that such precision allows for positional cloning of the markers and further provides guidance for the methods required to map a QTL with a precision of 1 cM.

15. Claims 54, 107, 253, and 262 are rejected under 35 U.S.C. 103(a) as being unpatentable over Aitman et al. in view of Manly et al. (cited as reference C75 in the Information Disclosure Statement filed 06 March 2006, Mammalian Genome Vol. 10, pages 327-334 (1999))

The claims are drawn to a method of measuring an expression quantitative trait locus (eQTL), a clinical quantitative trait locus (cQTL), and determining whether the gene assayed in the determination of the eQTL and the clinical trait are associated by determining if the eQTL and cQTL map to the same locus. In some embodiments the claims are computer programs or computers that execute the process. In some embodiments the mapping utilizes regression or interval mapping, or maximum likelihood analysis.

Art Unit: 1631

Aitman et al. shows in the abstract a method of genetically analyzing complex disorders such as diabetes by correlating a QTL for different traits of diabetes (insulin-mediated glucose uptake and catecholamine-mediated lipolysis) with mapping of the expression trait for the gene Cd36. Aitman et al. used spontaneously hypertensive rat (SHR) animals as the phenotype that was mapped by both eQTL and cQTL. Aitman et al. maps insulin-mediated glucose uptake and catecholamine-mediated lipolysis to a region near the microsatellite marker D4Bro1 on pages 76-77, which is a determination of a cQTL. Figure 2 and the discussion on pages 77-78 show the analysis of cDNA by expression level microarrays that determines an eQTL that correlates with SHR individuals. The identified eQTL is from the Cd36 gene. Cd36 is mapped to a region near the D4Bro1 site in figures 3 and pages 78-79 (using radiation hybrids to a precision of about 1cM with a Lod of 5.1 to 9.6 for the intervals measured). Aitman et al. employs F2 crossed rats to map insulin-mediated glucose uptake and catecholamine-mediated lipolysis on page 79 to Cd36, which is a determination of a cQTL that colocalizes with the eQTL determined on page 78. Page 79 and figure 7 show that Cd36 mutations correlate with the trait and that a normal and an affected strain differ by a duplication or deletion of the Cd36 gene. Figure 1 and column 1 on page 77 show that the phenotype in affected individuals has partial penetrance in affecting glucose uptake.

Aitman et al. discuss on page 82 the use of a computer program termed MAPMAKER, but Aitman et al. does not provide details of their genetic mapping calculations.

Manly et al. reviews computer software for use in QTL analysis. Manly et al. shows in the second column of page 327 that two methods widely used are least squares regression and maximum likelihood estimation. Manly et al. also discusses use of interval mapping on pages

Art Unit: 1631

327-328 for use in QTL mapping. Manly et al. review a number of programs used for QTL mapping, including MAPMAKER (used by Aitman et al.) on pages 329-330.

It would have been obvious to a person of ordinary skill in the art at the time the invention was made to use a computer running the MAPMAKER program as shown in Aitman et al. because Manly et al. shows that MAPMAKER, as well as a number of other programs, are useful to map QTL markers. It would have been further obvious to use regression or maximum likelihood analysis, and additionally interval mapping because Manly et al. show that such analyses are useful to map QTL markers.

#### ***Response to Arguments***

16. Applicant's arguments filed 06 August 2009 have been fully considered but they are not persuasive. The applicants state that Aitman et al. does not disclose the limitation added by amendment that the first quantitative trait analysis (an identification of an eQTL) comprises testing for linkages between the plurality of expression statistics for said gene G and locations along a genetic map of the plurality of organisms. However as noted in the above rejections, Aitman et al. determines an eQTL on page 77 that is further mapped by radiation hybrid mapping using cell lines and by linkage analysis using HinfI RFLP analysis and backcross analysis using individual rats on pages 78-79. In total Aitman et al. does identify an eQTL that is mapped by linkage analysis, as required by the claims.

#### ***Conclusion***

17. **THIS ACTION IS MADE FINAL.** Applicant is reminded of the extension of time policy as set forth in 37 CFR 1.136(a).

Art Unit: 1631

A shortened statutory period for reply to this final action is set to expire THREE MONTHS from the mailing date of this action. In the event a first reply is filed within TWO MONTHS of the mailing date of this final action and the advisory action is not mailed until after the end of the THREE-MONTH shortened statutory period, then the shortened statutory period will expire on the date the advisory action is mailed, and any extension fee pursuant to 37 CFR 1.136(a) will be calculated from the mailing date of the advisory action. In no event, however, will the statutory period for reply expire later than SIX MONTHS from the mailing date of this final action.

18. Any inquiry concerning this communication or earlier communications from the examiner should be directed to John S. Brusca whose telephone number is 571 272-0714. The examiner can normally be reached on M-F 8:30 AM - 5:00 PM.

If attempts to reach the examiner by telephone are unsuccessful, the examiner's supervisor, Marjorie A. Moran can be reached on 571-272-0720. The fax phone number for the organization where this application or proceeding is assigned is 571-273-8300.

Information regarding the status of an application may be obtained from the Patent Application Information Retrieval (PAIR) system. Status information for published applications may be obtained from either Private PAIR or Public PAIR. Status information for unpublished applications is available through Private PAIR only. For more information about the PAIR system, see <http://pair-direct.uspto.gov>. Should you have questions on access to the Private PAIR system, contact the Electronic Business Center (EBC) at 866-217-9197 (toll-free). If you would like assistance from a USPTO Customer Service Representative or access to the automated information system, call 800-786-9199 (IN USA OR CANADA) or 571-272-1000.

Application/Control Number: 10/523,143  
Art Unit: 1631

Page 14

/John S. Brusca/

Primary Examiner, Art Unit 1631

jsb